

DEC 1 8 2001

TECH CENTER 1600/2900

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/847,809A

DATE: 11/29/2001

TIME: 14:05:27

Input Set : N:\Crf3\RULE60\09847809A.txt

Output Set: N:\CRF3\11292001\I847809A.raw

SEQUENCE LISTING

C--> (1) GENERAL INFORMATION:

(i) APPLICANT: Bandman, Olga

Hillman, Jennifer L.

Lal, Preeti

Corley, Neil C.

Shah, Purvi

(ii) TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

(B) STREET: 3174 Porter Drive

(C) CITY: Palo Alto

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/847,809A

(B) FILING DATE: 01-May-2001

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/270,270

(B) FILING DATE: 1999-03-16

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.

(B) REGISTRATION NUMBER: 36,749

(C) REFERENCE/DOCKET NUMBER: PF-0358 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555

(B) TELEFAX: 650-845-4166

(C) TELEX:

51 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: RATRNOT02

(B) CLONE: 922578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

ENTERED

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```

66      1              5              10              15
67 Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
68                20                25                30
69 Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
70                35                40                45
71 His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
72                50                55                60
73 Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
74                65                70                75                80
75 Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
76                85                90                95
77 Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
78                100               105               110
79 His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
80                115               120               125
81 Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
82                130               135               140
83 His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
84                145               150               155               160
85 Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
86                165               170               175
87 Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
88                180               185               190
89 His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
90                195               200               205
91 Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
92                210               215               220
93 Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
94                225               230               235               240
95 Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
96                245               250               255
97 Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
98                260               265               270
99 Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
100               275               280               285
101 Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
102               290               295               300
103 Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
104               305               310               315               320
105 Leu Thr Arg His His Asp Glu Leu
106               325

```

108 (2) INFORMATION FOR SEQ ID NO: 2:

110 (i) SEQUENCE CHARACTERISTICS:

111 (A) LENGTH: 1463 base pairs

112 (B) TYPE: nucleic acid

113 (C) STRANDEDNESS: single

114 (D) TOPOLOGY: linear

116 (vii) IMMEDIATE SOURCE:

117 (A) LIBRARY: RATRNOT02

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118      (B) CLONE: 922578
120      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
122      CGCAGAGCGG ACGTGGAGAG CGGACGNCAG CTGGATAACA GGGGACCGAT GATGTGGCGA      60
123      CCATCAGTTC TGCTGCTTCT GTTGCTACTG AGGCACGGGG CCCAGGGGAA GCCATCCCCA      120
124      GACGCAGGCC CTCATGGCCA GGGGAGGGTG CACCAGGCGG CCCCCCTGAG CGACGCTCCC      180
125      CATGATGACG CCCACGGGAA CTTCCAGTAC GACCATGAGG CTTTCCTGGG ACGGGAAGTG      240
126      GCCAAGGAAT TCGACCAACT CACCCAGAG GAAAGCCAGG CCCGTCTGGG GCGGATCGTG      300
127      GACCGCATGG ACCGCGCGGG GGACGGCGAG GGCTGGGTGT CGCTGGCCGA GCTTCGCGCG      360
128      TGGATCGCGC ACACGCAGCA GCGGCACATA CGGGACTCGG TGAGCGCGGC CTGGGACACG      420
129      TACGACACGG ACCGCGACGG GCGTGTGGGT TGGGAGGAGC TGCGCAACGC CACCTATGGC      480
130      CACTACGCGC CCGGTGAAGA ATTTTCATGAC GTGGAGGATG CAGAGACCTA CAAAAAGATG      540
131      CTGGCTCGGG ACGAGCGGCG TTTCCGGGTG GCCGACCAGG ATGGGGACTC GATGGCCACT      600
132      CGAGAGGAGC TGACAGCCTT CCTGCACCCC GAGGAGTTCC CTCACATGCG GGACATCGTG      660
133      ATTGCTGAAA CCCTGGAGGA CCTGGACAGA AACAAAGATG GCTATGTCCA GGTGGAGGAG      720
134      TACATCGCGG ATCTGTACTC AGCCGAGCCT GGGGAGGAGG AGCCGGCGTG GGTGCAGACG      780
135      GAGAGGCAGC AGTTCGGGA CTTCCGGGAT CTGAACAAGG ATGGGCACCT GGATGGGAGT      840
136      GAGGTGGGCC ACTGGGTGCT GCCCCCTGCC CAGGACCAGC CCCTGGTGGA AGCCAACCAC      900
137      CTGCTGCACG AGAGCGACAC GGACAAGGAT GGGCGGCTGA GCAAAGCGGA AATCCTGGGT      960
138      AATTGGAACA TGTTTGTGGG CAGTCAGGCC ACCAACTATG GCGAGGACCT GACCCGGCAC      1020
139      CACGATGAGC TGTGAGCACC GCGCACCTGC CACAGCCTCA GAGGCCCGCA CAATGACCGG      1080
140      AGGAGGGGCC GCTGTGGTCT GGCCCCCTCC CTGTCCAGGC CCCGCAGGAG GCAGATGCAG      1140
141      TCCAGGCAT CCTCCTGCCC CTGGGCTCTC AGGGACCCCC TGGGTCGGCT TCTGTCCCTG      1200
142      TCACACCCCC AACCCCAGGG AGGGGCTGTC ATAGTCCCAG AGGATAAGCA ATACCTATTT      1260
143      CTGACTGAGT CTCCAGCCC AGACCCAGGG ACCCTTGGCC CCAAGCTCAG CTCTAAGAAC      1320
144      CGCCCCAACC CCTCCAGCTC CAAATCTGAG CCTCCACCAC ATAGACTGAA ACTCCCCTGG      1380
145      CCCAGCCCT CTCCTGCCTG GCCTGGCCTG GGACACCTCC TCTCTGCCAG GAGGCAATAA      1440
146      AAGCCAGCGC CGGGAATAAAA AAA                                     1463
148      (2) INFORMATION FOR SEQ ID NO: 3:
150      (i) SEQUENCE CHARACTERISTICS:
151          (A) LENGTH: 315 amino acids
152          (B) TYPE: amino acid
153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY: linear
156      (vii) IMMEDIATE SOURCE:
157          (A) LIBRARY: BLADNOT03
158          (B) CLONE: 1601793
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
162      Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
163      1          5          10          15
164      Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
165      20          25          30
166      Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
167      35          40          45
168      His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
169      50          55          60
170      Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
171      65          70          75          80
172      Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
173      85          90          95

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```

174 Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
175           100           105           110
176 Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
177           115           120           125
178 Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
179           130           135           140
180 Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
181           145           150           155           160
182 Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
183           165           170           175
185 Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
186           180           185           190
187 Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
188           195           200           205
189 Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
190           210           215           220
191 Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
192           225           230           235           240
193 Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp
194           245           250           255
195 Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
196           260           265           270
197 Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
198           275           280           285
199 Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp
200           290           295           300
201 Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe
202           305           310           315

```

204 (2) INFORMATION FOR SEQ ID NO: 4:

206 (i) SEQUENCE CHARACTERISTICS:

207 (A) LENGTH: 2658 base pairs

208 (B) TYPE: nucleic acid

209 (C) STRANDEDNESS: single

210 (D) TOPOLOGY: linear

212 (vii) IMMEDIATE SOURCE:

213 (A) LIBRARY: BLADNOT03

214 (B) CLONE: 1601793

216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

218 CCCGCTTCCG GTTGGGCGGT GCTTGCGCGC GTGAGCTGAG CCGGTGGGTG AGCGGCGGCC      60
219 ACGGCATCCT GTGCTGTGGG GGCTACGAGG AAAGATCTAA TTATCATGGA CCTGCGACAG      120
220 TTTCTTATGT GCCTGTCCCT GTGCACAGCC TTTGCCTTGA GCAAACCCAC AGAAAAGAAG      180
221 GACCGTGTAC ATCATGAGCC TCAGCTCAGT GACAAGGTTC ACAATGATGC TCAGAGTTTT      240
222 GATTATGACC ATGATGCCTT CTTGGGTGCT GAAGAAGCAA AGACCTTTGA TCAGCTGACA      300
223 CCAGAAGAGA GCAAGGAAAG GCTTGGAAAG ATTGTAAGTA AAATAGATGG CGACAAGGAC      360
224 GGGTTTGTCA CTGTGGATGA GCTCAAAGAC TGGATTAAAT TTGCACAAAA GCGCTGGATT      420
225 TACGAGGATG TAGAGCGACA GTGGAAGGGG CATGACCTCA ATGAGGACGG CCTCGTTTCC      480
226 TGGGAGGAGT ATAAAAATGC CACCTACGGC TACGTTTTAG ATGATCCAGA TCCTGATGAT      540
227 GGATTTAAC TAAACAGAT GATGGTTAGA GATGAGCGGA GGTTTAAAT GGCAGACAAG      600
228 GATGGAGACC TCATTGCCAC CAAGGAGGAG TTCACAGCTT TCCTGCACCC TGAGGAGTAT      660

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229 GACTACATGA AAGATATAGT AGTACAGGAA ACAATGGAAG ATATAGATAA GAATGCTGAT 720
230 GGTTCATTG ATCTAGAAGA GTATATTGGT GACATGTACA GCCATGATGG GAATACTGAT 780
231 GAGCCAGAAAT GGGTAAAGAC AGAGCGAGAG CAGTTTGTTG AGTTTCGGGA TAAGAACCGT 840
232 GATGGGAAGA TGGACAAGGA AGAGACCAAA GACTGGATCC TTCCCTCAGA CTATGATCAT 900
233 GCAGAGGCAG AAGCCAGGCA CCTGGTCTAT GAATCAGACC AAAACAAGGA TGGCAAGCTT 960
234 ACCAAGGAGG AGATCGTTGA CAAGTATGAC TTATTTGTTG GCAGCCAGGC CACAGATTTT 1020
235 GGGGAGGCC TTAGTACGCA TGATGAGTTC TGAGCTACGG AGGAACCCTC ATTTCCCTCAA 1080
236 AAGTAATTTA TTTTACAGC TTCTGGTTTC ACATGAAATT GTTTGCGCTA CTGAGACTGT 1140
237 TACTACAAAC TTTTAAAGAC ATGAAAAGGC GTAATGAAAA CCATCCCGTC CCCATTCCCTC 1200
238 CTCTCTCTG AGGGACTGGA GGGGAGCCGT GCTTCTGAGG AACCACTCTA ATTAGTACAC 1260
239 TTGTGTTTGT AGATTTACAC TTTGTATTAT GTATTAACAT GGCGTGTTTA TTTTGTATT 1320
240 TTTCTCTGGT TGGGAGTATG ATATGAAGGA TCAAGATCCT CAACTCACAC ATGTAGACAA 1380
241 ACATTAGCTC TTTACTCTTT CTCAACCCCT TTTATGATTT TAATAATTCT CACTTAACTA 1440
242 ATTTTGTAAG CCTGAGATCA ATAAGAAATG TTCAGGAGAG AGGAAAGAAA AAAAATATAT 1500
243 GCTCCACAAT TTATATTTAG AGAGAGAACA CTTAGTCTTG CCTGTCAAAA AGTCCAACAT 1560
244 TTCATAGGTA GTAGGGGCCA CATATTACAT TCAGTTGCTA TAGGTCCAGC AACTGAACCT 1620
245 GCCATTACCT GGGCAAGGAA AGATCCCTTT GCTCTAGGAA AGCTTGCCCC AAATTGATTT 1680
246 TCTTCTTTT CCCCTGTAG GACTGACTGT TGGCTAATTT TGTCAAGCAC AGCTGTGGTG 1740
247 GGAAGAGTTA GGGCCAGTGT CTTGAAAATC AATCAAGTAG TGAATGTGAT CTCTTTCAG 1800
248 AGCTATAGAT AGAAACAGCT GGAAAACATA AGGAAAAATA CAAATGTTTT CGGGGCATAC 1860
249 ATTTTTTTTC TGGGTGTGCA TCTGTTGAAA TGCTCAAGAC TTAATTATTT GCCTTTTGAA 1920
250 ATCACTGTAA ATGCCCCCAT CCGGTTCCCTC TTCTTCCCAG GTGTGCCAAG GAATTAATCT 1980
251 TGGTTTCACT ACAATTAAAA TTCACTCCTT TCCAATCATG TCATTGAAAAG TGCTTTTAA 2040
252 GAAAGAAATG GTCACTGAAT GGAATTTCTC TTAAGAAACC CTGAGATTAA AAAAAGACTA 2100
253 TTTGGATAAC TTATAGGAAA GCCTAGAACC TCCCAGTAGA GTGGGGATTT TTTTCTTCT 2160
254 CCCTTCTCT TTTGGACAAT AGTTAAATTA GCAGTATTAG TTATGAGTTT GGTGTCAGTG 2220
255 TTCTTATCTT GTGGGCTGAT TTCCAAAAAC CACATGCTGC TGAATTTACC AGGATCCTC 2280
256 ATACCTCACA ATGCAAACCA CTTACTACCA GGCTTTTTC TGTGTCCACT GGAGAGCTTG 2340
257 AGCTCACACT CAAAGATCAG AGGACCTACA GAGAGGGCTC TTTGGTTTGA GGACCATGGC 2400
258 TTACCTTTCC TGCTTTTGAC CCATCACACC CCATTTCCCT CTCTTTCCCT CTCCCCGCTG 2460
259 CCAAAAAAAA AAAAAAAGGA AACGTTTATC ATGAATCAAC AGGGTTTCAG TCCTTATCAA 2520
260 AGAGAGATGT GGAAAGAGCT AAAGAAACCA CCCTTTGTTT CCAACTCCAC TTTACCCATA 2580
261 TTTTATGCAA CACAAACACT GTCCTTTTGG GTCCCTTCTT TACAGATGGG ACCTCTTGAG 2640
262 GAAGGAATTA TCGTATTC 2658

```

264 (2) INFORMATION FOR SEQ ID NO: 5:

266 (i) SEQUENCE CHARACTERISTICS:

267 (A) LENGTH: 331 amino acids

268 (B) TYPE: amino acid

269 (C) STRANDEDNESS: single

270 (D) TOPOLOGY: linear

272 (vii) IMMEDIATE SOURCE:

273 (A) LIBRARY: GenBank

274 (B) CLONE: 1262329

276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

278 Met Ala Arg Gly Gly Arg Gly Arg Arg Gly Leu Ala Leu Gly Leu

279 1 5 10 15

280 Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr

281 20 25 30

282 Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg

VERIFICATION SUMMARY

DATE: 11/29/2001

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TIME: 14:05:28

Input Set : N:\Crf3\RULE60\09847809A.txt

Output Set: N:\CRF3\11292001\I847809A.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]